

RAW SEQUENCE LISTING DATE: 05/10/2000
PATENT APPLICATION: US/09/558,474 TIME: 16:39:28

Input Set : A:\758k1-00.app
Output Set: N:\CRF3\05092000\I558474.raw

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4 (1) GENERAL INFORMATION:
5
6 (i) APPLICANT: Bazan, J. Fernando
7
8 (ii) TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
9
10 (iii) NUMBER OF SEQUENCES: 16
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: DNAX Research Institute
14 (B) STREET: 901 California Avenue
15 (C) CITY: Palo Alto
16 (D) STATE: California
17 (E) COUNTRY: USA
18 (F) ZIP: 94304-1104
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
C--> 26 (vi) CURRENT APPLICATION DATA:
C--> 27 (A) APPLICATION NUMBER: US/09/558,474
C--> 28 (B) FILING DATE: 25-Apr-2000
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: US 60/053,765
33 (B) FILING DATE: 25-JUL-1997
34
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: Ching, Edwin P.
37 (B) REGISTRATION NUMBER: 34,090
38 (C) REFERENCE/DOCKET NUMBER: DX0758K1
39
40 (ix) TELECOMMUNICATION INFORMATION:
41 (A) TELEPHONE: (650)852-9196
42 (B) TELEFAX: (650)496-1200
43
44 (2) INFORMATION FOR SEQ ID NO: 1:
45
46 (i) SEQUENCE CHARACTERISTICS:
47 (A) LENGTH: 570 base pairs
48 (B) TYPE: nucleic acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear
51
52 (ii) MOLECULE TYPE: cDNA
53
54 (ix) FEATURE:
55 (A) NAME/KEY: CDS
56 (B) LOCATION: 1..567
57
58 (ix) FEATURE:
59 (A) NAME/KEY: mat_peptide
60 (B) LOCATION: 64..567
61
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
63
64 ATG CTG GGG AGC AGA GCT GTA ATG CTG CTG TTG CTG CTG CCC TGG ACA
65 Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Pro Trp Thr
66
67 -21 -20 -15 -10

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71 GCT CAG GGC AGA GCT GTG CCT GGG GGC AGC AGC CCT GCC TGG ACT CAG      96
72 Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln
73 -5      1      5      10
75 TGC CAG CAG CTT TCA CAG AAG CTC TGC ACA CTG GCC TGG AGT GCA CAT      144
76 Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His
77      15      20      25
79 CCA CTA GTG GGA CAC ATG GAT CTA AGA GAA GAG GGA GAT GAA GAG ACT      192
80 Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr
81      30      35      40
83 ACA AAT GAT GTT CCC CAT ATC CAG TGT GGA GAT GGC TGT GAC CCC CAA      240
84 Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln
85      45      50      55
87 GGA CTC AGG GAC AAC AGT CAG TTC TGC TTG CAA AGG ATC CAC CAG GGT      288
88 Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly
89 60      65      70      75
91 CTG ATT TTT TAT GAG AAG CTG CTA GCA TCC CAT ATT TTC ACA GGG GAG      336
92 Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu
93      80      85      90
95 CCT TCT CTG CTC CCT GAT AGC CCT GTG GCG CAG CTT CAT GCC TCC CTA      384
96 Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu
97      95      100      105
99 CTG GGC CTC AGC CAA CTC CTG CAG CCT GAG GGT CAC CAC TGG GAG ACT      432
100 Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr
101      110      115      120
103 CAG CAG ATT CCA AGC CTC AGT CCC AGC CAG CCA TGG CAG CGT CTC CTT      480
104 Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu
105      125      130      135
107 CTC CGC TTC AAA ATC CTT CGC AGC CTC CAG GCC TTT GTG GCT GTA GCC      528
108 Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala
109 140      145      150      155
111 GCC CGG GTC TTT GCC CAT GGA GCA GCA ACC CTG AGT CCC TAA      570
112 Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro
113      160      165

116 (2) INFORMATION FOR SEQ ID NO: 2:
118 (i) SEQUENCE CHARACTERISTICS:
119 (A) LENGTH: 189 amino acids
120 (B) TYPE: amino acid
121 (D) TOPOLOGY: linear
123 (ii) MOLECULE TYPE: protein
125 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
127 Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Leu Pro Trp Thr
128 -21 -20      -15      -10
130 Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln
131 -5      1      5      10
133 Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His
134      15      20      25
136 Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr
137      30      35      40
139 Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln

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140      45      50      55
142 Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly
143 60      65      70      75
145 Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu
146      80      85      90
148 Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu
149      95      100      105
151 Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr
152      110      115      120
154 Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu
155      125      130      135
157 Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala
158 140      145      150      155
160 Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro
161      160      165
163 (2) INFORMATION FOR SEQ ID NO: 3:
165 (i) SEQUENCE CHARACTERISTICS:
166 (A) LENGTH: 1203 base pairs
167 (B) TYPE: nucleic acid
168 (C) STRANDEDNESS: single
169 (D) TOPOLOGY: linear
171 (ii) MOLECULE TYPE: cDNA
174 (ix) FEATURE:
175 (A) NAME/KEY: CDS
176 (B) LOCATION: 113..700
178 (ix) FEATURE:
179 (A) NAME/KEY: mat_peptide
180 (B) LOCATION: 176..700
183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
185 CGCTTAGAAG TCGGACTACA GAGTTAGACT CAGAACC AAA GGAGGTGGAT AGGGGGTCCA 60
187 CAGGCCTGGT GCAGATCACA GAGCCAGCCA GATCTGAGAA GCAGGGAACA AG ATG 115
188 Met
189 -21
191 CTG GAT TGC AGA GCA GTA ATA ATG CTA TGG CTG TTG CCC TGG GTC ACT 163
192 Leu Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val Thr
W--> 193 -20      -15      -10      -5
195 CAG GGC CTG GCT GTG CCT AGG AGT AGC AGT CCT GAC TGG GCT CAG TGC 211
196 Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln Cys
W--> 197      1      5      10
199 CAG CAG CTC TCT CGG AAT CTC TGC ATG CTA GCC TGG AAC GCA CAT GCA 259
200 Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His Ala
201      15      20      25
203 CCA GCG GGA CAT ATG AAT CTA AGA GAA GAA GAG GAT GAA GAG ACT 307
204 Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu Thr
205      30      35      40
207 AAA AAT AAT GTG CCC CGT ATC CAG TGT GAA GAT GGT TGT GAC CCA CAA 355
208 Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro Gln
209 45      50      55      60
211 GGA CTC AAG GAC AAC AGC CAG TTC TGC TTG CAA AGG ATC CGC CAA GGT 403

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```

212 Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln Gly
213          65          70          75
215 CTG GCT TTT TAT AAG CAC CTG CTT GAC TCT GAC ATC TTC AAA GGG GAG      451
216 Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly Glu
217          80          85          90
219 CCT GCT CTA CTC CCT GAT AGC CCC ATG GAG CAA CTT CAC ACC TCC CTA      499
220 Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser Leu
221          95          100          105
223 CTA GGA CTC AGC CAA CTC CTC CAG CCA GAG GAT CAC CCC CGG GAG ACC      547
224 Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu Thr
225          110          115          120
227 CAA CAG ATG CCC AGC CTG AGT TCT AGT CAG CAG TGG CAG CGC CCC CTT      595
228 Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro Leu
229          125          130          135          140
231 CTC CGT TCC AAG ATC CTT CGA AGC CTC CAG GCC TTT TTG GCC ATA GCT      643
232 Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile Ala
233          145          150          155
235 GCC CGG GTC TTT GCC CAC GGA GCA GCA ACT CTG ACT GAG CCC TTA GTG      691
236 Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu Val
237          160          165          170
239 CCA ACA GCT TAAGGATGCC CAGGTTCCCA TGGCTACCAT GATAAGACTA      740
240 Pro Thr Ala
241          175
243 ATCTATCAGC CCAGACATCT ACCAGTTAAT TAACCCATTA GGACTTGTGC TGTCTTGTG      800
245 TCGTTTGTGTT TGGGTGAAGG GCAAGGACAC CATTATTAAA GAGAAAAGAA ACAAACCCCA      860
247 GAGCAGGCAG CTGGCTAGAG AAAGGAGCTG GAGAAGAAGA ATAAAGTCTC GAGCCCTGG      920
249 CCTTGAAGC GGGCAAGCAG CTGCGTGCCG TGAGGGGAAG GGGGCGGTGG CATCGAGAAA      980
251 CTGTGAGAAA ACCCAGAGCA TCAGAAAAAG TGAGCCCAGG CTTGGCCAT TATCTGTAAG      1040
253 AAAAAACAAGA AAAGGGGAAC ATTACTTTT CCTGGGTGGC TCAGGGAAAT GTGCAGATGC      1100
255 ACAGTACTCC AGACAGCAGC TCTGTACCTG CCTGCTCTGT CCCTCAGTTC TAACAGAATC      1160
257 TAGTCACTAA GAACTAACAG GACTACCAAT ACGAACTGAC AAA      1203
260 (2) INFORMATION FOR SEQ ID NO: 4:
262 (i) SEQUENCE CHARACTERISTICS:
263 (A) LENGTH: 196 amino acids
264 (B) TYPE: amino acid
265 (D) TOPOLOGY: linear
267 (ii) MOLECULE TYPE: protein
269 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
271 Met Leu Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val
272 -21 -20          -15          -10
274 Thr Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln
275 -5          1          5          10
277 Cys Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His
278          15          20          25
280 Ala Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu
281          30          35          40
283 Thr Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro
284          45          50          55
286 Gln Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln

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287 60          65          70          75
289 Gly Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly
290          80          85          90
292 Glu Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser
293          95          100          105
295 Leu Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu
296          110          115          120
298 Thr Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro
299          125          130          135
301 Leu Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile
302 140          145          150          155
304 Ala Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu
305          160          165          170
307 Val Pro Thr Ala
308          175
310 (2) INFORMATION FOR SEQ ID NO: 5:
312 (i) SEQUENCE CHARACTERISTICS:
313 (A) LENGTH: 102 amino acids
314 (B) TYPE: amino acid
315 (C) STRANDEDNESS: not relevant
316 (D) TOPOLOGY: linear
318 (ii) MOLECULE TYPE: peptide
323 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
325 Ser Cys Leu Gln Arg Ile His Gln Gly Leu Val Phe Tyr Glu Lys Leu
326 1 5 10 15
328 Leu Gly Ser Asp Ile Phe Thr Gly Glu Pro Ser Leu His Pro Asp Gly
329 20 25 30
331 Ser Val Gly Gln Leu His Ala Ser Leu Leu Gly Leu Arg Gln Leu Leu
332 35 40 45
334 Gln Pro Glu Gly His His Trp Glu Thr Glu Gln Thr Pro Ser Pro Ser
335 50 55 60
337 Pro Ser Gln Pro Trp Gln Arg Leu Leu Leu Arg Leu Lys Ile Leu Arg
338 65 70 75 80
340 Ser Leu Gln Ala Phe Val Ala Val Ala Ala Arg Val Phe Ala His Gly
341 85 90 95
343 Ala Ala Thr Leu Ser Gln
344 100
346 (2) INFORMATION FOR SEQ ID NO: 6:
348 (i) SEQUENCE CHARACTERISTICS:
349 (A) LENGTH: 174 amino acids
350 (B) TYPE: amino acid
351 (C) STRANDEDNESS: not relevant
352 (D) TOPOLOGY: linear
354 (ii) MOLECULE TYPE: peptide
359 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
361 Thr Pro Leu Gly Pro Ala Arg Ser Leu Pro Gln Ser Phe Leu Leu Lys
362 1 5 10 15
364 Cys Leu Glu Gln Val Arg Lys Ile Gln Ala Asp Gly Ala Glu Leu Gln
365 20 25 30

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VERIFICATION SUMMARY
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TIME: 16:39:29

Input Set : A:\758k1-00.app
Output Set: N:\CRF3\05092000\I558474.raw

L:193 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:197 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3